This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Computational models			
Bioinformatics-based approach to identify combined microRNA- and mRNA-derived cancer signatures	A bioinformatics approach to predict mRNA and miRNA connectivity in transcriptional networks could help identify genetic vulnerabilities in cancer cells. The method analyzes mRNA and miRNA expression data based on transcript abundance and fold changes. The method was used to generate a thermodynamic signature comprised of about 100 genes that could distinguish tumor cells from normal cells. The signature highlighted a network of connected mRNAs and miRNAs that is strengthened in cancer cells but not in normal cells. Next steps include using the approach to predict patient-specific tumor differences. SciBX 6(43); doi:10.1038/scibx.2013.1237 Published online Nov. 7, 2013	Patent status undisclosed; licensing status not applicable	Zadran, S. <i>et al. Proc. Natl. Acad. Sci. USA</i> ; published online Oct. 7, 2013; doi:10.1073/pnas.1316991110 Contact: R.D. Levine, The Hebrew University of Jerusalem, Jerusalem, Israel e-mail: rafi@fh.huji.ac.il